WHAT IS CLAIMED IS:

1. A method for determining a methylation profile of a cell, tissue or organism, the method comprising the steps of:

a. providing a uniform population of randomly cleaved or sheared DNA from the cell or organism, wherein the DNA comprises a first portion and a second portion and each portion comprises methylated and unmethylated nucleotides;

b. separating the second portion into a methylated DNA sub-portion and a methylated DNA sub-portion;

c. quantifying the relative amount of at least one specific sequence in at least two DNA samples selected from the group consisting of the first portion, the methylated DNA sub-portion, and the unmethylated DNA sub-portion,

thereby determining the methylation profile of several such nucleic acid sequences from a cell, tissue or organism.

2. The method of claim 1, wherein the method comprises the steps of:

labeling the at least two DNA samples with different labels, and

hybridizing the at least two DNA samples to a nucleic acid; and

determining the relative hybridization of the at least two DNA samples to the specific sequence by calculating the ratio of the two hybridizing labels.

3. The method of claim 1, wherein the quantifying step comprises quantitative amplification.

4. The method of claim 1, wherein the at least two DNA samples are the methylated DNA sub-portion and the unmethylated DNA sub-portion.

5. The method of claim 1, wherein the at least two DNA samples are the first portion and the methylated DNA sub-portion.

6. The method of claim 1, wherein the at least two DNA samples are the first portion and the unmethylated DNA sub-portion.

7. The method of claim 1, wherein the randomly cleaved or sheared DNA comprises methylated and unmethylated recognition sequences of a methyl-sensitive

restriction enzyme and the separating step comprises cleaving the second portion with the methyl-sensitive restriction enzyme.

8. The method of claim 1, wherein the randomly cleaved or sheared DNA comprises methylated and unmethylated recognition sequences of a methyl-dependent restriction enzyme and the separating step comprises cleaving the second portion with the methyl-dependent restriction enzyme.

9. The method of claim 2, wherein the nucleic acid is linked to a solid support.

10. The method of claim 9, wherein the solid support is a microarray.

11. The method of claim 9, wherein the solid support is a bead.

12. The method of claim 9, wherein the solid support is a matrix.

13. The method of claim 1, wherein the organism is a plant.

14. The method of claim 1, wherein the organism is a fungus.

15. The method of claim 1, wherein the organism is a prokaryote.

16. The method of claim 15, wherein the prokaryote is a bacterial pathogen.

17. The method of claim 16, wherein the bacterial pathogen is selected from the group consisting of gram positive and gram negative species and mycobacteria..

18. The method of claim 1, wherein the organism is an animal.

19. The method of claim 18, wherein the animal is a human.

20. The method of claim 1, wherein the cell is a stem cell.

21. The method of claim 1, wherein the cell is transgenic and the nucleic acid corresponds to the insertion site of a transgene.

22. The method of claim 1, whereinthe tissue is blood.

23. The method of claim 1, wherein the tissue is biopsy tissue.

24. The method of claim 1, wherein the tissue is resected tissue.

25. The method of claim 1, wherein the tissue is normal.

26. The method of claim 1, wherein the tissue is precancerous.

27. The method of claim 1, wherein the cell is transgenic and the nucleic acid corresponds to the insertion site of a transgene. In some embodiments, the tissue is blood. In some embodiments, the tissue is biopsy tissue. In some embodiments, the tissue is resected tissue. In some embodiments, the tissue is normal.

28. The method of claim 1, further comprising comparing the methylation profile of a nucleic acid with the transcription of the nucleic acid, thereby determining the relation between methylation and transcription of the nucleic acid.

29. The method of claim 28, wherein the transcription of the nucleic acid is detected with a microarray.

30. The method of claim 1, further comprising comparing the methylation profile of a specimen of a bacterial pathogen with a reference strain of the pathogen, wherein similarity of the methylation patterns indicates common origin of the specimen and the reference strain.

31. A polynucleotide microarray hybridizing to first and a second labeled DNA portions, wherein the portions are from uniform populations of randomly cleaved or sheared DNA from a cell or organism;

wherein the first DNA portion comprises unmethylated and methylated DNA labeled with a first label; and

wherein the second DNA portion is depleted for either unmethylated DNA or methylated DNA and the second portion of DNA is labeled with a second label different from the first label.

32. The polynucleotide microarray of claim 31, wherein the second test DNA portion is depleted for methylated DNA.

33. The polynucleotide microarray of claim 31, wherein the second test DNA portion is depleted for unmethylated DNA.

34. The polynucleotide microarray of claim 31, wherein the second DNA portion is depleted by

treating the randomly cleaved or sheared DNA with a methyl-sensitive or a methyl-dependent restriction enzyme and

selecting uncleaved DNA.

35. The polynucleotide microarray of claim 31, where the DNA populations are from a plant.

36. The polynucleotide microarray of claim 31, where the DNA populations are from an animal.

37. The polynucleotide microarray of claim 31, where the DNA populations are from a fungus.

38. The polynucleotide microarray of claim 31, where the DNA populations are from a prokaryote.

39. The polynucleotide microarray of claim 38, wherein the prokaryote is a bacterial pathogen.

40. The polynucleotide microarray of claim 39, wherein the bacterial pathogen is selected from the group consisting of *Listeria*, *E. coli*, *Salmonella*, *Yersinia*, and *Neisseria*.

41. The polynucleotide microarray of claim 31, where the DNA populations are from a transgenic organism or cell.

42. The polynucleotide microarray of claim 31, the polynucleotide microarray comprises gene promoters and/or polynucleotide sequences which when methylated, silence neighboring gene expression.

43. A method for producing an epigenetically uniform or diverse population of progeny from one or more parent individuals, the method comprising the steps of:

a. determining the genomic methylation profile of sexually or asexually propagated progeny of a parent individual; and

b. selecting progeny exhibiting a uniform or diverse methylation profile, thereby producing an epigenetically uniform population from one or more parent individuals.

44. The method of claim 43, further comprising determining the methylation profile of a parent individual and the selecting step comprises selecting progeny that exhibit the methylation profile of the parent individual.

45. The method of claim 44, wherein the parent is an F1 hybrid.

46. The method of claim 43, wherein the progeny are sexually propagated.

47. The method of claim 43, wherein the progeny are asexually propagated.

48. The method of claim 43, wherein the parent individual is a plant.

49. The method of claim 43, wherein the parent individual is an animal.

50. The method of claim 43, wherein the parent individual is a fungus.

51. The method of claim 43, wherein the parent individual is a prokaryote.

52. The method of claim 43, wherein the progeny are clones of the parent.

53. The method of claim 43, wherein the genomic methylation profile is determined on a solid support.

54. The method of claim 53, wherein the solid support is a membrane.

55. The method of claim 53, wherein the solid support is a methyl binding column.

56. The method of claim 53, wherein the solid support is a microarray.

57. The method of claim 53, wherein the solid support is a bead.

58. The method of claim 43, wherein the determining step comprises separating a randomly cleaved or sheared uniform DNA population into methylated and unmethylated fractions;
labeling the methylated or unmethylated fractions with a first label; and
hybridizing the methylated or unmethylated fractions to a nucleic acid.

59. The method of claim 58, wherein the method further comprises providing total genomic DNA labeled with a second label and hybridizing the total genomic DNA to a nucleic acid, thereby normalizing the signal from the first label.

60. The method of claim 43,wherein the randomly cleaved or sheared DNA comprises methylated and unmethylated recognition sequences of a methyl-sensitive restriction enzyme and the depleting step comprises cleaving the second portion with the methyl-sensitive restriction enzyme.

61. The method of claim 43, wherein the randomly cleaved or sheared DNA comprises methylated and unmethylated recognition sequences of a methyl-dependent restriction enzyme and the depleting step comprises cleaving the second portion with the methyl-dependent restriction enzyme.

62. The method of claim 43, wherein progeny are screened in groups.

63. A method of associating heterosis with methylation profiles, the method comprising,
crossing individuals to produce progeny;
determining the methylation profile of the individuals and the progeny; and
comparing a trait of the progeny with the methylation profiles of the individuals, thereby associating appearance of the trait with a methylation profile.

64. The method of claim 63, wherein the individuals are from different heterotic groups.